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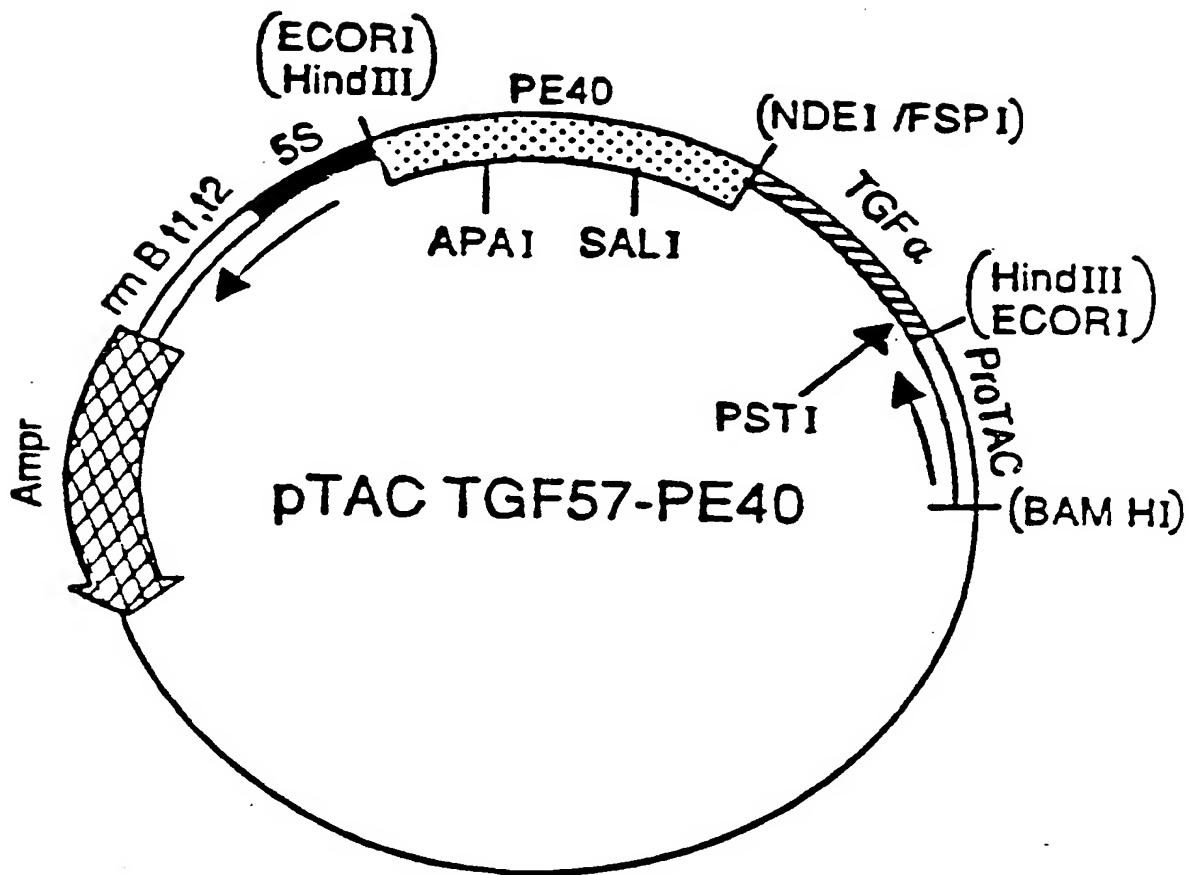
(54) Method of treating bladder cancer cells.

(57) We have modified PE₄₀ toxin by removing at least two of its four cysteine amino acid residues and have formed hybrid molecules containing modified PE₄₀ linked to TGF-alpha and have found that these hybrid molecules have utility in killing bladder cancer cells.

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FIGURE 1



BACKGROUND OF THE INVENTION

Traditional cancer chemotherapy relies on the ability of drugs to kill tumor cells in cancer patients. Unfortunately, these same drugs frequently kill normal cells as well as the tumor cells. The extent to which a cancer drug kills tumor cells rather than normal cells is an indication of the compound's degree of selectivity for tumor cells. One method of increasing the tumor cell selectivity of cancer drugs is to deliver drugs preferentially to the tumor cells while avoiding normal cell populations. Another term for the selective delivery of chemotherapeutic agents to specific cell populations is "targeting". Drug targeting to tumor cells can be accomplished in several ways. One method relies on the presence of specific receptor molecules found on the surface of tumor cells. Other molecules, referred to as "targeting agents", can recognize and bind to these cell surface receptors. These "targeting agents" include, e.g., antibodies, growth factors, or hormones. "Targeting agents" which recognize and bind to specific cell surface receptors are said to target the cells which possess those receptors. For example, bladder tumor cells possess a protein on their surfaces called the epidermal growth factor receptor. Transforming growth factor-alpha (TGF-alpha) recognizes and binds to the EGF receptor on bladder tumor cells. TGF-alpha is therefore, a "targeting agent" for these tumor cells.

"Targeting agents" by themselves do not kill tumor cells. Other molecules including cellular poisons or toxins can be linked to "targeting agents" to create hybrid molecules that possess both tumor cell targeting and cellular toxin domains. These hybrid molecules function as tumor cell selective poisons by virtue of their abilities to target tumor cells and then kill those cells via their toxin component. Some of the most potent cellular poisons used in constructing these hybrid molecules are bacterial toxins that inhibit protein synthesis in mammalian cells. *Pseudomonas exotoxin A* is one of these bacterial toxins, and has been used to construct hybrid "targeting - toxin" molecules (U.S. Patent 4,545,985).

Pseudomonas exotoxin A intoxicates mammalian cells by first binding to the cell's surface, then entering the cell cytoplasm and inactivating elongation factor 2 which is a cellular protein required for protein synthesis. *Pseudomonas exotoxin A* has been used to construct anticancer hybrid molecules using monoclonal antibodies and protein hormones. However, one problem with these hybrid molecules is that they exhibit toxicity towards normal cells. At least part of the toxicity associated with hybrid molecules containing *pseudomonas exotoxin A* is due to the ability of *pseudomonas exotoxin A* by itself to bind to and enter many types of mammalian cells. Therefore, hybrid molecules formed between *pseudomonas exotoxin A* and specific "targeting agents" can bind to many normal cells in addition to the cells recognized by the "targeting agent". One method of dealing with this problem is to modify *pseudomonas exotoxin A* so that it is no longer capable of binding to normal cells. This can be accomplished by removing that portion of the *pseudomonas exotoxin A* molecule which is responsible for its cellular binding activity. A truncated form of the *pseudomonas exotoxin A* molecule has been prepared which retains the ability to inactivate elongation factor 2 but no longer is capable of binding to mammalian cells. This modified *pseudomonas exotoxin A* molecule is called *pseudomonas exotoxin - 40* or PE₄₀ (Hwang, et al., Cell 48:129-136 1987).

PE₄₀ has been linked to several targeting molecules including TGF-alpha (Chaudhary, et al., PNAS USA 84:4583-4542 1987). In the case of TGF-alpha, hybrid molecules containing PE₄₀ and TGF-alpha domains are capable of specifically binding to tumor cells that possess EGF receptors and intoxicating these cells via inhibiting protein synthesis. In order for this hybrid molecule to efficiently bind to the EGF receptor it must assume the proper conformation. Efficient receptor binding is also dependent on having the "targeting domain" properly exposed so that it is accessible for binding. When TGF-alpha and PE₄₀ hybrid molecules are produced as fusion proteins in bacteria using recombinant DNA techniques the majority of hybrid molecules exhibit poor EGF receptor binding activity.

DISCLOSURE STATEMENT

1. U.S. patent 4,545,985 teaches that *pseudomonas exotoxin A* can be chemically conjugated to an antibody or to epidermal growth factor. While this patent further teaches that these conjugates can be used to kill human tumor cells, these chemically linked toxins have been shown to have undesirable, nonspecific levels of activity.
2. U.S. Patent 4,664,911 teaches that antibodies can be conjugated to the A chain or the B chain of ricin which is a toxin obtained from plants. Patent 4,664,911 further teaches that these conjugates can be used to kill human tumor cells.
3. U.S. Patent 4,675,382 teaches that hormones such as melanocyte stimulating hormone (MSH) can be linked to a portion of the diphtheria toxin protein via peptide bonds. Patent 4,675,382 further teaches that the genes which encode these proteins can be joined together to direct the synthesis of a hybrid fusion protein using recombinant DNA techniques. This fusion protein has the ability to bind to cells that possess

MSH receptors.

5. Murphy, et al., PNAS USA 83:8258-8262 1986, Genetic construction, expression, and melanoma-selective cytotoxicity of a diphtheria toxin-related alpha-melanocyte-stimulating hormone fusion protein. This article teaches that a hybrid fusion protein produced in bacteria using recombinant DNA technology and consisting of a portion of the diphtheria toxin protein joined to alpha-melanocyte-stimulating hormone will bind to and kill human melanoma cells.

10. Allured, et al., PNAS USA 83:1320-1324 1986, Structure of exotoxin A of *Pseudomonas aeruginosa* at 3.0 Angstrom. This article teaches the three dimensional structure of the *pseudomonas* exotoxin A protein.

15. Hwang, et al., Cell 48:129-136 1987, Functional Domains of *Pseudomonas* Exotoxin Identified by Deletion Analysis of the Gene Expressed in *E. Coli*. This article teaches that the *pseudomonas* exotoxin A protein can be divided into three distinct functional domains responsible for: binding to mammalian cells, translocating the toxin protein across lysosomal membranes, and ADP ribosylating elongation factor 2 inside mammalian cells. This article further teaches that these functional domains correspond to distinct regions of the *pseudomonas* exotoxin A protein.

20. Chaudhary, et al., PNAS USA 84:4538-4542 1987, Activity of a recombinant fusion protein between transforming growth factor type alpha and *Pseudomonas* toxin. This article teaches that hybrid fusion proteins formed between PE-40 and transforming growth factor-alpha and produced in bacteria using recombinant DNA techniques will bind to and kill human tumor cells possessing epidermal growth factor receptors.

25. European patent application 0 261 671, published 30 March 1988, teaches that a portion of the *pseudomonas* exotoxin A protein can be produced which lacks the cellular binding function of the whole *pseudomonas* exotoxin A protein but possesses the translocating and ADP ribosylating functions of the whole *pseudomonas* exotoxin A protein. The portion of the *pseudomonas* exotoxin A protein that retains the translocating and ADP ribosylating functions of the whole *pseudomonas* exotoxin A protein is called pseudomonas exotoxin - 40 or PE-40. PE-40 consists of amino acid residues 252-613 of the whole *pseudomonas* exotoxin A protein as defined in Gray, et al., PNAS USA 81:2645-2649 1984. This patent application further teaches that PE-40 can be linked to transforming growth factor-alpha to form a hybrid fusion protein produced in bacteria using recombinant DNA techniques.

30. Kelley, et al., PNAS USA 85:3980-3984 1988, Interleukin 2-diphtheria toxin fusion protein can abolish cell-mediated immunity in vivo. This article teaches that a hybrid fusion protein produced in bacteria using recombinant DNA technology and consisting of a portion of the diphtheria toxin protein joined to interleukin 2 functions in mice to suppress cell mediated immunity.

35. Bailon, Biotechnology, pp. 1326-1329 Nov. 1988. Purification and Partial Characterization of an Interleukin 2-*Pseudomonas* Exotoxin Fusion Protein. This article teaches that hybrid fusion proteins formed between PE-40 and interleukin 2 and produced in bacteria using recombinant DNA techniques will bind to and kill human cell lines possessing interleukin 2 receptors.

40. Edwards, et al., Mol. Cell. Biol. 9: 2860-2867 1989 describe the preparation of the modified TGF-alpha - PE₄₀ hybrid molecules that have been found to have utility in treating bladder tumor cells.

45. Heimbrook, et al., Proc. Natl. Acad. Sci. USA 87: 4697-4701 1990 describe the *in vivo* efficacy of modified TGF-alpha - PE₄₀ in significantly prolonging the survival of mice containing human tumor cell xenografts.

OBJECTS OF THE INVENTION

It is an object of the present invention to provide modifications of PE₄₀ which permit efficient binding of hybrid molecules formed between TGF-alpha and modified PE₄₀ molecules to cellular receptors on bladder tumor cells that recognize the TGF-alpha "targeting agent". It is another object of this invention to provide a method for selectively killing bladder tumor cells. A further object is to provide a hybrid molecule of enhanced potency formed between TGF-alpha and modified PE₄₀ molecules. Another object of the present invention is to provide pharmaceutical compositions containing as active ingredient a hybrid molecule containing a PE₄₀ domain (or region) wherein the PE₄₀ domain has been modified to improve binding of the hybrid protein to the epidermal growth factor receptor on bladder tumor cells. These and other objects of the present invention will be apparent from the following description.

55 SUMMARY OF INVENTION

The present invention provides a hybrid molecule comprising a modified PE₄₀ domain bonded to a TGF-alpha targeting domain. The modified PE₄₀ domain improves the receptor binding activity of this hybrid

molecule. Substitution of other neutral amino acids such as, e.g., alanine, for the cysteine residues in PE₄₀, or deletion of cysteine residues, improves binding of the hybrid molecule to the receptors recognized by the targeting domain. The hybrid molecules of the present invention bind more efficiently to targeted receptors on human tumor cells than hybrid molecules having unmodified PE₄₀, and have utility in killing bladder tumor cells.

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DETAILED DESCRIPTION OF THE INVENTION

Hybrid molecules formed between TGF-alpha and PE₄₀ are characterized in three primary assay systems. These assays include: 1 - ADP ribosylation of elongation factor 2 which measures the enzymatic activity of TGF-alpha - PE₄₀ that inhibits mammalian cell protein synthesis, 2 - inhibition of radiolabeled EGF binding to the EGF receptor on membrane vesicles from A431 cells which measures the EGF receptor binding activity of TGF-alpha - PE₄₀, and 3 - cell proliferation as assessed by conversion of 3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetrazolium bromide (MTT) to formazan which is used to measure the survival of tumor cells following exposure to TGF-alpha - PE₄₀. These assays are performed as previously described (Dominic, *et al.*, Infection and Immunity 16:832-841 1977, Cohen *et al.*, J. Biol. Chem. 257:1523-1531 1982, Riemen, *et al.*, Peptides 8:877-885 1987, Mosmann J. Immunol Methods 65:55-63 1983).

To create new TGF-alpha - PE₄₀ hybrid molecules with superior receptor binding characteristics we first produced a series of recombinant DNA molecules that encoded either TGF-alpha - PE₄₀ or specifically modified versions of TGF-alpha - PE₄₀. The original or parental TGF-alpha - PE₄₀ gene was molecularly cloned in a bacterial TAC expression plasmid vector (pTAC TGF57-PE40) using distinct segments of cloned DNA as described in Example 1. The pTAC TGF57-PE40 DNA clone was used as the starting reagent for constructing specifically modified versions of TGF-alpha - PE₄₀ DNA. The specific modifications of the pTAC TGF57-PE40 DNA involve site-specific mutations in the DNA coding sequence required to replace two or four of the cysteine codons within the PE₄₀ domain of the pTAC TGF57-PE40 DNA with codons for other amino acids. Alternatively, the site specific mutations can be engineered to delete two or four of the cysteine codons within the PE40 domain of pTAC TGF57-PE40. The site specific mutations in the pTAC TGF57-PE40 DNA were constructed using the methods of Winter, *et al.*, Nature 299:756-758 1982. Specific examples of the mutated pTAC TGF57-PE40 DNAs are presented in Example 3. The amino acid sequence of the hybrid protein encoded by the pTAC TGF57-PE40 DNA is presented in Table 2. The four cysteine residues in the PE₄₀ domain of the parental TGF-alpha - PE₄₀ hybrid protein are designated residues Cys²⁶⁵, Cys²⁸⁷, Cys³⁷², and Cys³⁷⁹ (Table 2). Amino acid residues in the PE₄₀ domain are numbered as defined in Gray, *et al.*, PNAS USA 81: 2645-2649 (1984). The modified TGF-alpha - PE₄₀ hybrid proteins generated from the specifically mutated pTAC TGF57-PE40 DNA contain substitutions or deletions of the two N-terminal PE₄₀ residues [Cys²⁶⁵ and Cys²⁸⁷] or the two C-terminal residues [Cys³⁷² and Cys³⁷⁹], or both [Cys²⁶⁵, Cys²⁸⁷, Cys³⁷², and Cys³⁷⁹]. To simplify the nomenclature for describing the modified hybrid proteins produced from these mutated pTAC TGF57-PE40 DNAs we have designated the amino acid residues at the N-terminal positions the "A" locus and the residues at the C-terminal positions the "B" locus. When cysteine residues are present at the two N-terminal PE₄₀ positions as in parental TGF-alpha - PE₄₀ hybrid molecule, the locus is capitalized (i.e. "A"). When these cysteines are substituted with other neutral amino acids such as, for example, glycine, alanine, phenylalanine, valine, leucine, isoleucine, tyrosine, histidine, tryptophan, serine, threonine or methionine, or deleted from the N-terminal positions, the locus is represented by a lower case "a". Similarly, if the amino acid residues at the two C-terminal positions are cysteines the locus is represented by an upper case "B" while a lower case "b" represents this locus when the amino acid residues at these positions are substituted with other amino acids or deleted. Thus when all four cysteine residues in the PE₄₀ domain of TGF-alpha - PE₄₀ are substituted with alanines the modified hybrid protein is designated TGF-alpha - PE₄₀ ab. In a similar fashion the parental TGF-alpha - PE₄₀ hybrid protein with cysteines at amino acid residue positions 265, 287, 372 and 379 can be designated TGF-alpha - PE₄₀ AB.

Both the TGF-alpha - PE₄₀ AB hybrid protein and the modified TGF-alpha - PE₄₀ hybrid proteins are produced in *E. coli* using the TAC expression vector system described by Linemeyer, *et al.*, Bio-Technology 5:960-965 1987. The recombinant hybrid proteins produced in these bacteria are harvested and purified by lysing the bacteria in guanidine hydrochloride followed by the addition of sodium sulphite and sodium tetrathionate. This reaction mixture is subsequently dialyzed and urea is added to solubilize proteins that have precipitated out of solution. The mixture is next centrifuged to remove insoluble proteins and the recombinant hybrid TGF-alpha - PE₄₀ proteins are separated using ion exchange chromatography followed by size exclusion chromatography, followed once again by ion exchange chromatography. The purified TGF-alpha - PE₄₀ hybrid proteins are next exposed to reducing agents such as beta-mercaptoethanol in order to permit disulfide bonds to form within the hybrid protein between pairs of cysteine residues. Finally, the refolded hybrid proteins are subjected to size exclusion and ion exchange chromatography to isolate highly pure TGF-alpha - PE₄₀ protein. The precise details of this purification scheme are described in Example 4. Once purified and refolded the biologic activity

of these hybrid proteins can be characterized using the ADP ribosylation, EGF receptor binding, and cell proliferation assays described above.

Alternatively, and preferably, the hybrid proteins TGF-alpha - PE₄₀ AB, TGF-alpha - PE₄₀ Ab, TGF-alpha - PE₄₀ aB and TGF-alpha - PE₄₀ ab are produced in transformed bacteria. The bacteria are harvested and the cell paste is lysed and treated, preferably by centrifugation, to remove debris and undesired proteins. The desired hybrid protein then is precipitated by addition of a sulfite salt, preferably (NH₄)₂SO₄, to the supernatant liquid. The precipitate is sulfitolysed, refolded by addition of excess β-mercaptoethanol, concentrated and separated by ion-exchange chromatography and metal-chelating chromatography. Specific details are disclosed in Example 5.

An important utility of TGF-alpha modified PE₄₀ lies in its ability to bind to and kill human bladder tumor cells. The anti-cancer proteins described herein have utility in killing bladder cancer cells and are used for this purpose in the form of a solution or suspension in a physiologically acceptable liquid such as, for example, sterile water, water for injection, saline or, preferably, buffered saline or buffered saline containing a carrier protein such as, for example, human serum albumin, e.g., phosphate buffered saline or PBS containing human serum albumin. The solution or suspension contains from about 0.1 mg to about 10 mg of anti-cancer hybrid protein per 60 ml of physiologically acceptable liquid. More preferably, it contains from about 0.5 mg to about 5 mg per 60 ml, and most preferably, it contains from about 2 mg to about 4 mg per 60 ml of physiologically acceptable liquid.

The method of the present invention consists in contacting the bladder cancer cells with the solution or suspension containing the anti-cancer proteins described herein for a period of from less than an hour, for example, about 30 minutes, to a period of several hours, for example, up to about four hours, at ambient temperature. In the case of laboratory animals the solution or suspension is administered via a trans-urethral catheter.

While the use of TGF-alpha modified PE₄₀ hybrid molecules is described herein and in the following examples, it is to be understood that the scope of the present invention includes as targeting agents TGF-alpha, EGF, other members of the EGF family of peptide hormones that bind to the EGF receptor on bladder tumor cells, Shope fibroma virus growth factor, and vaccinia virus growth factor and that the toxin to which the targeting agent is coupled also includes PE₄₀, diphtheria toxin, ricin toxin or other members of the ADP-ribosylating class of mammalian cell poisons.

The following examples illustrate the present invention without, however, limiting the same thereto. All of the enzymatic reactions required for molecular biology manipulations, unless otherwise specified, were carried out as described in Maniatis, et al. (1982) In: Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press.

Example 1

Construction of recombinant DNA clones containing TGF-alpha - PE₄₀ DNA

The TGF-alpha DNA segment was constructed using three sets of synthetic oligonucleotides as described by Defeo-Jones, et al., Molecular and Cellular Biology 8:2999-3007 1988. This synthetic TGF-alpha gene was cloned into pUC-19. DNA from the pUC-19 clone containing recombinant human TGF-alpha was digested with Sph I and Eco RI. The digestion generated a 2.8 kb DNA fragment containing all of pUC-19 and the 5' portion of TGF-alpha. The 2.8 kb fragment was purified and isolated by gel electrophoresis. An Eco RI to Sph I oligonucleotide cassette was synthesized. This synthetic cassette had the sequence indicated below:

45

5' - CGGACCTCCTGGCTGCGCATCTAGG-3'
3' - GTACGCCTGGAGGACCGACGCGTAGATCCTTAA-5'

50

For convenience, this oligonucleotide cassette was named 57. Cassette 57 was annealed and ligated to the TGF-alpha containing 2.8 kb fragment forming a circularized plasmid. Clones which contained the cassette were identified by hybridization to radiolabeled cassette 57 DNA. The presence of human TGF-alpha was confirmed by DNA sequencing. Sequencing also confirmed the presence of a newly introduced Fsp I site at the 3' end of the TGF-alpha sequence. This plasmid, named TGF-alpha-57/pUC-19, was digested with HinD III and Fsp I which generated a 168 bp fragment containing the TGF-alpha gene (TGF-alpha-57). A separate preparation of pUC-19 was digested with HinD III and Eco RI which generated a 2.68 kb pUC-19 vector DNA. The PE₄₀ DNA was isolated from plasmid pVC 8 (Chaudhary, et al., PNAS USA 84:4538-4542 1987). pVC 8 was

digested using Nde I. A flush end was then generated on this DNA by using the standard conditions of the Klenow reaction (Maniatis, *et al.*, *supra*, p.113). The flush-ended DNA was then subjected to a second digestion with Eco RI to generate a 1.3 kb Eco RI to Nde I (flush ended) fragment containing PE₄₀. The TGF-alpha-57 HinD III to Fsp I fragment (168 bp) was ligated to the 2.68 kb pUC-19 vector. Following overnight incubation, 5 the 1.3 kb EcoRI to Nde I (flush ended) PE₄₀ DNA fragment was added to the ligation mixture. This second ligation was allowed to proceed overnight. The ligation reaction product was then used to transform JM 109 cells. Clones containing TGF-alpha-57 PE₄₀ in pUC-19 were identified by hybridization to radiolabeled TGF-alpha-57 PE₄₀ DNA and the DNA from this clone was isolated. The TGF-alpha-57 PE₄₀ was removed from the 10 pUC-19 vector and transferred to a TAC vector system described by Linemeyer, *et al.*, Bio-Technology 5:960-965 1987). The TGF-alpha-57 PE₄₀ in pUC-19 was digested with HinD III and Eco RI to generate a 1.5 kb fragment containing TGF-alpha-57 PE₄₀. A flush end was generated on this DNA fragment using standard Klenow reaction conditions (Maniatis, *et al.*, *loc. cit.*). The TAC vector was digested with HinD III and Eco RI. A flush 15 end was generated on the digested TAC vector DNA using standard Klenow reaction conditions (Maniatis, *et al.*, *loc. cit.*). The 2.7 kb flush ended vector was isolated using gel electrophoresis. The flush ended TGF-alpha-57 PE₄₀ fragment was then ligated to the flush ended TAC vector. The plasmid generated by this ligation was used to transform JM 109 cells. Candidate clones containing TGF-alpha-57 PE₄₀ were identified by hybridization as indicated above and sequenced. The clone containing the desired construction was named pTAC TGF57-PE40. The plasmid generated by these manipulations is depicted in Figure 1. The nucleotide sequence of the amino acid codons of the TGF-alpha - PE₄₀ fusion protein encoded in the pTAC TGF-57-PE40 DNA are 20 depicted in Table 1. The amino acid sequence encoded by the TGF-57-PE40 gene is shown in Table 2.

Example 2

25 Construction of modified versions of recombinant TGF-alpha - PE₄₀ containing DNA clones: Substitution of alanines for cysteines.

TGF-alpha - PE₄₀ aB:

30 The clone pTAC TGF57-PE40 was digested with SphI and BamHI and the 748 bp SphI-BamHI fragment (specifying the C-terminal 4 amino acids of TGF-alpha, 4 linker amino acids and the N-terminal 240 amino acids of PE₄₀) was isolated. M13 mp19 vector DNA was cut with SphI and BamHI and the vector DNA was isolated. The 748 bp SphI-BamHI TGF-alpha - PE₄₀ fragment was ligated into the M13 vector DNA overnight at 15°C. Bacterial host cells were transformed with this ligation mixture, candidate clones were isolated and their plasmid DNA was sequenced to insure that these clones contained the proper recombinant DNAs. Single stranded DNA 35 was prepared for mutagenesis.

An oligonucleotide (oligo #132) was synthesized and used in site directed mutagenesis to introduce a HpaI site into the TGF-alpha - PE₄₀ DNA at amino acid position 272 of PE₄₀:

5' CTGGAGACGTTAACCCGTC 3' (oligo #132)

40 One consequence of this site directed mutagenesis was the conversion of residue number 272 in PE₄₀ from phenylalanine to leucine. The mutagenesis was performed as described by Winter, *et al* Nature, 299:756-758 1982.

45 A candidate clone containing the newly created HpaI site was isolated and sequenced to validate the presence of the mutated genetic sequence. This clone was then cut with SphI and SalI. A 198 bp fragment specifying the C-terminal 5 amino acids of TGF-alpha and the N-terminal 61 amino acids of PE₄₀ and containing the newly introduced HpaI site was isolated and subcloned back into the parent pTAC TGF57-PE40 plasmid at the SphI-SalI sites. Bacterial host cells were transformed, a candidate clone was isolated and its plasmid DNA was sequenced to insure that this clone contained the proper recombinant DNA. For convenience this clone was 50 named pTAC TGF57-PE40-132. pTAC TGF57-PE40-132 was digested with SphI and HpaI and a 3.96 Kb DNA fragment was isolated. A synthetic oligonucleotide cassette (oligo #153) spanning the C-terminal 5 amino acids of TGF-alpha and the N-terminal 32 amino acids of PE₄₀ and containing SphI and HpaI compatible ends was synthesized and ligated to the digested pTAC TGF57-PE40-132:

5' CGGACCTCTGGCCATGGCGAAGAGGGCGGCAGCCTGGCCGCGCTGACCGCGCA
 3' GTACGCCCTGGAGGACCGGTACCGGCTTCTCCCGCGTGGACCGCGCGACTGGCGCGT

5 CCAGGCTGCACACCTGCCGCTGGAGAGTT 3'
 GGTCCGACGTGTGGACGGGACCTCTGCAA 5' (oligo #153)

10 This oligonucleotide cassette incorporated a change in the TGF-alpha - PE₄₀ DNA so that the codon specifying alanine at residue 51 was eliminated and the codon specifying cysteine at residue 264 of PE₄₀ now specified alanine. For convenience this plasmid DNA was called pTAC TGF57-PE40-132,153. Bacterial host cells were transformed with pTAC TGF57-PE40-132, 153 DNA. Candidate clones were identified by hybridization, isolated and their plasmid DNA was sequenced to insure that it contained the proper recombinant DNA.

15 pTAC TGF57-PE40-132,153 DNA was digested with HpaI and Sall and a 3.95 Kb vector DNA was isolated. A synthetic oligonucleotide cassette (oligo #142) spanning amino acid residues 272 to 309 of PE₄₀ and containing HpaI and Sall compatible ends was synthesized and ligated to the 3.95 Kb pTAC TGF/PE40 132,153 DNA.

20 5' AACCCGTATGCCAGCCGCGCGCTGGAAACAACCTGGAGCAGGCTGGCTATCCGGTGC
 3' TTGGGCAGTAGCGGTGGCGCGCCGACCCCTTGTGACCTCGTCCGACCGATAAGGCCACG
 AGCGGCTGGTCGCCCTCTACCTGGCGGCCGCGCTGTCTGGAAACCAGG 3'
 25 TCGCCGACCAGCGGGAGATGGACCGCCGCCGACAGCACCTGGTCCAGCT 5' (oligo #142)

30 This oligonucleotide cassette changed the codon specifying cysteine at residue 287 so that this codon now specified alanine. For convenience this mutated plasmid DNA was called pTAC TGF57-PE40-132,153,142. Bacterial host cells were transformed with this plasmid and candidate clones were identified by hybridization. These clones were isolated and their plasmid DNA was sequenced to insure that it contained the proper recombinant DNA. The pTAC TGF57-PE40-132,153,142 plasmid encodes the TGF-alpha - PE₄₀ variant with both N-terminal cysteines at locus "A" replaced by alanines. Therefore, following the nomenclature described previously this modified version of TGF-alpha - PE₄₀ is called TGF-alpha - PE₄₀ aB. The amino acid sequence encoded by the TGF-alpha-PE₄₀ aB gene is shown in Table 3.

35 TGF-alpha - PE₄₀ Ab:

The clone pTAC TGF57-PE40 was digested with SphI and BamHI and the 748 bp SphI-BamHI fragment (specifying the C-terminal 4 amino acids of TGF-alpha 4 linker amino acids and the N-terminal 240 amino acids of PE₄₀) was isolated. M13 mp19 vector DNA was cut with SphI and BamHI and the vector DNA was isolated. The 748 bp SphI-BamHI TGF-alpha - PE₄₀ fragment was ligated into the M13 vector DNA overnight at 15°C. Bacterial host cells were transformed with this ligation mixture, candidate clones were isolated and their plasmid DNA was sequenced to insure that these clones contained the proper recombinant DNAs. Single stranded DNA was prepared for mutagenesis.

45 An oligonucleotide (oligo #133) was synthesized and used in site directed mutagenesis to introduce a BstEII site into the TGF-alpha - PE₄₀ DNA at amino acid position 369 of PE₄₀:

5' GACGTGGTGACCCCTGAC 3' (oligo #133)

50 One consequence of this mutagenesis was the conversion of the serine residue at position 369 of PE₄₀ to a threonine.

A DNA clone containing the newly created BstEII site was identified, isolated and sequenced to ensure the presence of the proper recombinant DNA. This clone was next digested with Apal and Sall restriction enzymes. A 120 bp insert DNA fragment containing the newly created BstEII site was isolated and ligated into pTAC TGF57-PE40 that had also been digested with Apal and Sall. Bacterial host cells were transformed, and a candidate clone was isolated and sequenced to insure that the proper recombinant DNA was present. This newly created plasmid DNA was called pTAC TGF57-PE40-133. It was digested with BstEII and Apal and 2.65 Kb vector DNA fragment was isolated.

A BstI to Apal oligonucleotide cassette (oligo #155) was synthesized which spanned the region of TGF-alpha - PE₄₀ deleted from the pTAC TGF57-PE40-133 clone digested with BstI and Apal restriction enzymes. This cassette also specified the nucleotide sequence for BstI and Apal compatible ends.

5 5' GTGACCCCTGACCGCGCCGGTCGCCGCCGGTGAAGCTGCAGGGCC 3'
 3' GGACTGGCGCGGCCAGCGCGGCCACTTCGACGC 5' (oligo #155)

This oligonucleotide cassette changed the codons for cysteines at residues 372 and 379 of PE₄₀ to codons specifying alanines. Oligonucleotide cassette #155 was ligated to the 2.65 Kb vector DNA fragment. Bacterial host cells were transformed and candidate clones were isolated and sequenced to insure that the proper recombinant DNA was present. This newly created DNA clone was called pTAC TGF57-PE40-133,155. It encodes the TGF-alpha - PE₄₀ variant with both cysteines at locus "B" replaced by alanines. Therefore, following the nomenclature described previously this modified version of TGF-alpha - PE₄₀ is called TGF-alpha - PE₄₀ Ab.

15 The amino acid sequence encoded by the TGF-alpha-PE₄₀ Ab gene is shown in Table 4.

TGF-alpha - PE₄₀ ab:

The pTAC-TGF57-PE40-132,153,142 plasmid encoding TGF-alpha - PE₄₀ ab was digested with Sall and Apal and the resultant 3.8 Kb vector DNA fragment was isolated. The pTAC TGF57-PE40-133,155 plasmid encoding TGF-alpha - PE₄₀ Ab was also digested with Sall and Apal and the resultant 140 bp DNA fragment containing the cysteine to alanine changes at amino acid residues 372 and 379 of PE₄₀ was isolated. These two DNAs were ligated together and used to transform bacterial host cells. Candidate clones were identified by hybridization with a radiolabeled 140 bp DNA from pTAC TGF57-PE40-133,155. Plasmid DNA from the candidate clones was isolated and sequenced to insure the presence of the proper recombinant DNA. This newly created DNA clone was called pTAC TGF57-PE40-132,153,142,133,155. This plasmid encodes the TGF-alpha - PE₄₀ variant with all four cysteines at loci "A" and "B" replaced by alanines. Therefore, following the nomenclature described previously this modified version of TGF-alpha - PE₄₀ is called TGF-alpha - PE₄₀ ab. The amino acid sequence encoded by the TGF-alpha-PE₄₀ ab gene is shown in Table 5.

30 Example 3

Construction of modified versions of recombinant TGF-alpha-PE₄₀ containing DNA clones: Deletion of cysteine residues

35 TGF-alpha-PE₄₀ ab, TGF-alpha-PE₄₀ Ab, and TGF-alpha-PE₄₀ ab can also be constructed by removing the cysteine residues at locus "A" and/or locus "B". Construction of these versions of TGF-alpha-PE₄₀ are accomplished identically as described in Example 3 except that: for TGF-alpha-PE₄₀ ab oligonucleotide cassette 153 is changed such that the alanine codon intended for position 265 is deleted and oligonucleotide cassette 142 is changed such that the alanine codon intended for position 287 is deleted. For TGF-alpha-PE₄₀ Ab oligonucleotide cassette 155 is changed such that the alanine codons intended for residues 372 and 379 are deleted. For TGF-alpha-PE₄₀ ab the DNA fragments used to construct this recombinant gene are taken from the TGF-alpha-PE₄₀ ab and TGF-alpha-PE₄₀ Ab gene described in this example.

45 EXAMPLE 4

Production and isolation of recombinant TGF-alpha- PE₄₀ fusion proteins:

Production of fusion Protein

50 Transformed *E. coli* JM-109 cells were cultured in 1L shake flasks in 500 ml LB-Broth in the presence of 100 mg/ml ampicillin at 37°C. After the A600 spectrophotometric absorbance value reached 0.6, isopropyl B-D-thiogalactopyranoside was added to a final concentration of 1 mM. After 2 hours the cells were harvested by centrifugation.

S-Sulphonation of fusion protein

The cells were lysed in 8M guanidine hydrochloride, 50 mM Tris pH 8.0, 1 mM EDTA by stirring at room

temperature for 2 hours. The lysis mixture was brought to 0.4 M sodium sulphite and 0.1M sodium tetrathionate by adding solid reagents and the pH was adjusted to 9.0 with 1M NaOH. The reaction was allowed to proceed at room temperature for 16 hours.

5 Preparation for chromatography

The protein solution was dialysed against a 10,000 fold excess volume of 1mM EDTA at 4°C. The mixture was then brought to 6M urea, 50 mM Tris pH 8.0, 50 mM NaCl at room temperature and stirred for 2 hours. Any undissolved material was removed by centrifugation at 32,000 x g for 30 minutes.

10 DEAE F.F. Sepharose Chromatography

15 The cleared supernatant from the previous step was applied to a 26 x 40 cm DEAE Fast Flow column (Pharmacia LKB Biotechnology Inc.) equilibrated with 6M urea, 50 mM Tris pH 8.0, 50 mM NaCl at a flow rate of 1 ml/minute. The column was washed with the equilibration buffer until all unabsorbed materials were removed as evidenced by a UV 280 spectrophotometric absorbance below 0.1 in the equilibration buffer as it exits the column. The adsorbed fusion protein was eluted from the column with a 1000 ml 50-350 mM NaCl gradient and then concentrated in a stirred cell Amicon concentrator fitted with a YM-30 membrane.

20 Sephacryl S-300

25 The concentrated fusion protein (8 mls) was applied to a 2.6 x 100 cm Sephadryl S-300 column (Pharmacia LKB Biotechnology- Inc.) equilibrator with 6M urea, 50 mM Tris pH 8.0, 50 mM NaCl at a flow rate of 0.25 ml/minute. The column was eluted with additional equilibration buffer and 3 ml fractions collected. Fractions containing TGF-alpha - PE₄₀ activity were pooled.

Q-sepharose Chromatography

30 The pooled fractions from the S-300 column were applied to a 1.6 x 40 cm Q-sepharose column (Pharmacia LKB Biotechnology, Inc.) equilibrated with 6M urea, 50 mM Tris pH 8.0, 50 mM NaCl at a flow rate of 0.7 ml/minute. The column was washed with the equilibration buffer and then eluted with a 600 ml 50-450 mM NaCl gradient. The fractions containing the TGF-alpha - PE₄₀ activity were pooled and then dialysed against 50 mM glycine pH 9.0 and stored at -20°C.

35 Refolding

40 A sample of the protein was thawed and diluted to a spectrophotometric absorbance at UV A280 = 0.1 in 50 mM glycine pH 10.5. Beta-mercaptoethanol was added to give a 4:1 molar ratio over the theoretical number of S-sulphonate groups present in the protein sample. The reaction was allowed to proceed for 16 hours at 4°C after which time the solution was dialysed against a 10,000 fold excess of physiologically buffered saline and stored at -20°C.

EXAMPLE 5

45 Production and Isolation of Recombinant TGF-alpha - PE₄₀ Fusion Proteins

50 E. coli strain JM-109, containing the appropriate TGF-alpha - PE₄₀ plasmid, was cultured at 37°C in complex medium (Bauer, *et al.*, Biotechnology and Bioengineering **16** 933-41 (1974)) with antibiotic at 100 mg/ml. TGF-PE₄₀ expression was induced upon addition of 1 mM isopropylthiogalactoside after the culture had attained an absorbance at 600 nm of 2.5. The culture was harvested by cross-flow filtration following a nine hour induction period, and frozen at -70°C.

55 The cell paste was thawed on ice in 4 volumes of 50 mM sodium phosphate, pH 7.8, to form a suspension that was passed through 4 layers of cheesecloth and then twice through a Matin-Gaulin press at 9,000 psi. The filtered suspension was centrifuged in a Sorvall GS-3 rotor at 9000 rpm (13,000 x g) for 30 minutes to remove debris. Saturated ammonium sulfate solution was added to the supernatant liquid dropwise with stirring to a 20% saturation (250 ml/l) at room temperature. The suspension was stirred at 4°C for 0.5 - 1 hour and then centrifuged in the GS-3 rotor at 9000 rpm (13,000 x g) for 20 minutes.

Saturated ammonium sulfate was added to the supernatant liquid with stirring to a 35% concentration (230

ml/l supernatant). The ammonium sulfate containing solution was stirred at 4°C for 0.5 - 1 hour and then centrifuged as above. The pellet was resuspended in 50 mM sodium phosphate, 50% NH₄SO₄ pH 7.5 at 1/4 of the starting volume, stirred as above and centrifuged in the Sorvall SA-600 at 5,000 rpm (3,600 x g) for 15 minutes in polypropylene tubes. The supernatant liquid was discarded and the pellets resuspended at 10 mg protein/ml in 50 mM Tris, 6M guanidine-HCl, pH 9.0 at room temperature.

5 Na₂SO₃ was added to a concentration of 0.4M and Na₂S₄O₆ was added to a concentration of 0.1M. The pH was checked; if not 9.0, an appropriate adjustment is made with HCl or NaOH. After stirring overnight at room temperature, the sulfitolyzed protein was dialyzed exhaustively against 50 mM Gly-Cl, pH 9.0 at 4°C.

10 The protein was then diluted to 0.1 mg/ml in 50 mM Gly-Cl, pH 10.5 and a 40-fold molar excess of β-mercaptoethanol (87 mM β-Me at 0.1 mg/ml) was added. The mixture was stirred at 4°C for about 15 hours, and the refolded protein was dialyzed for about 15 hours at 4°C against 20 mM Tris-Cl, 50 mM NaCl, pH 8.0. The protein was then loaded onto a Q-Sepharose column pre-equilibrated in 20 mM Tris-Cl, 50 mM NaCl, pH 8.0, at 4°C, using about 0.3 ml resin/mg protein, and eluted with a linear salt gradient from 50 mM to 500 mM NaCl in 20 mM Tris-Cl, pH 8.0 (gradient size = 6 - 10 column volumes).

15 The column fractions were analyzed and pooled by A₂₈₀ UV absorption, gel electrophoresis and Western blots. A metal-chelating column was prepared by treating chelating sepharose 4B with CuSO₄ using 0.3 to 1 ml resin/mg protein. The column was equilibrated with 50 mM Tris-acetate, 1M NaCl, pH 7.0. To assure that no Cu²⁺ was eluting, a second metal-free column of chelating Sepahrose 4B was installed downstream of the Cu²⁺-charged column.

20 The Q-Sepharose sample pool was diluted 1:2 in 50 mM Tris-acetate, 1M NaCl, pH 7.0, and loaded onto the metal-chelating column at room temperature. The column was washed with one column volume of equilibration buffer, and the protein eluted with a linear gradient of 0 to 70 mM imidazole, maintained at pH 7.0, in the equilibration buffer (gradient size 10 to 40 column volumes).

25 The column fractions were analyzed and pooled by A₂₈₀ UV absorption, gel electrophoresis and Western blots.

EXAMPLE 6

30 Eight human bladder carcinoma cell lines were obtained from the American Type Culture Collection (ATCC) as frozen ampoules. They were immediately cultured and passaged as monolayers according to the instructions provided by ATCC. After characterizing the growth rate of each cell line, cells were plated in 96-well plates at the appropriate dilution to form sub-confluent layers in control wells at the end of the assay. The next day these sub-confluent cultures, maintained either on serum-free MEM-a, RPMI 1640 or McCoy's 5A medium, were utilized in a standard cell kill assay (Mosmann, J. Immunol. Methods 65: 55-63, 1983; Edwards et al., Mol. Cell. Biol. 9: 2860-2867, 1989). Each cell line was seeded into 96-well plates at 10,000 viable cells per well. Twenty-four hours later, the cells were washed once and placed in serum-free medium containing the test compound under study. Forty-eight hours later the number of surviving cells was quantitated by using an MTT [3-(3,4-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide] assay as described by Mosmann, *supra*. The activity of the toxin against each cell line was assessed, and the data are summarized in the following table, with activity 35 against A431 (vulva carcinoma) cells presented for comparison.

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50

Activity of TGF-alpha-PE40 ab (EX. 5)Against human Bladder Carcinoma Cell Lines

	<u>Cell Line</u>	<u>EC₅₀ (pM)*</u>
5	J-82	130
	RT-4	180
	5637	180
10	SCaBER	230
	UMUC-3	830
	T-24	840
	TCGSUP	7,000
	HT1197	11,500
15	A431	79

*concentration (picomoles/liter) that reduces number of cells surviving after 48 hours to 50% of number of control cells.

20

EXAMPLE 7Comparison of Several Cancer Cell Lines Against TGF-alpha - PE₄₀ AB, TGF-alpha - PE₄₀ ab of EX. 4 and TGF-alpha - PE₄₀ ab of EX. 5

		<u>EC₅₀'s [pM]</u>	<u>AB</u>	<u>(EX. 4)</u>	<u>(EX. 5)</u>
<u>SQUAMOUS CELL</u>					
30	A-431		39	378	163
	A-431		146	355	161
	A-431		94	314	183
	A-431		77	297	207
35	HeLa		8356	310088	3988
	SCC-4		227	861	445
	SCC-9		443	647	218
	SCC-15		106	392	193
	SCC-25		39	147	67
40	<u>GLIOBLASTOMA</u>				
	U138MG		20889	>316nM	216609
	U373MG		>316nM	>316nM	204064
45	<u>BREAST ADENOCARCINOMA</u>				
	MDA-MB-468		78	527	253
	BT-20		58	207	94
	MCF-7		>316nM	>316nM	>316nM
50	<u>COLON ADENOCARCINOMA</u>				
	HT-29		7605	786	669
<u>NORMAL CELL LINES</u>					
55	CHO		>316nM	>316nM	>316nM
	NR-6		>316nM	>316nM	>316nM

TABLE 1

5 ATGGCTGAGCAGTGGTGTCCCATTTAATGAATGCCAGATTCCACACTCAGTTCTGCTTCATGAAACATGCAGG
 TTTTGGTGCAGGAGGACAAGCCGGCATGTGCTGCCATTCTGGTACGTTGGTGCAGCGCTGTGAGCATGCAGGACCTC
 CTGGCTGCTATGGCCGAAGAGGGCGGAGCCTGGCCGGCTGACCGCGACCAGGCTTGCCACCTGCCGTGGAGACT
 TTACCCGTATGCCAGCCGCGGCTGGAAACACTGGAGCAGTGCCTGAGCCCTGGCCAGCCCCGGCAGCGGCGGC
 10 TACCTGGCGGCGGGCTGTCGTGAAACCAGGTCGACCAAGGTGATCCGCAACGCCCTGGCCAGCCCCGGCAGCGGCGGC
 GACCTGGGCAGAGCGATCCGAGCAGCGGAGCAGGCCCTGGCCCTGACCTGGCCGGCCGAGAGCGAGCGC
 TTCGTECGGCAGGGCACCGCAACGACGAGGCCGGCAGCGCAGGCGAACGCCGACGTGGTGAACCTGACCTGCCGGTCGC
 15 GCCGGTGAATGCGGGGCCGGGACAGCGCGACGCCCTGCTGGAGCGCAACTATCCCACTGGCGCGGAGTTCCCTC
 GGCGACGGCGGCGACGTCACTCAGCACCCGCGCACGCAACTGGACGGTGGAGCGCTGCTCCAGGCCACCGC
 CAACTGGAGGGAGCGGGCTATGTGTTGTCGGTACACGGCACCTCCTGAAAGCGGCGCAAAGCATGTCCTCGGC
 20 GGGGTGCGCGCGCAGGCCAGGACCTCGACCGATCTGGCGCGGTTCTATATCGCCGGGATCCGGCGCTGGCCTAC
 GGCTACGCCAGGACCAAGGAACCCGACGCCAGCGGCCGGATCCGCAACGGTGCCCTGCTGGGGCTATGTGCCGCG
 TCGAGCCCTGCCGGCTTCTACCGCACCGCCCTGACCTGGCCGGCGGGAGGCAGGCGGGCGAGGTGAAACGGCTGATC
 25 GGCCATCCGCTGCCGCTGCCCTGGACGCCATCACGGCCCCGAGGAGGAAGGCGGGCGCTGGAGACCAATTCTCGGC
 TGGCCGCTGGCGAGCGCACCGTGGTATTCCCTCGCGATCCCCACCGACCCGGCAACGTGGCGGCGACCTCGAC
 CCGTCCAGCATCCCCGACAAGGAACAGGCAGTCAAGGCCCTGCCGGACTACGCCAGCCAGCCCCGGCAAACCGCCGCG
 GAGGACCTGAAGTAA

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TABLE 2TGF-alpha-PE₄₀ AMINO ACID SEQUENCE

5	-4 -3 -2 -1' TGFA'	6	16
	Met Ala Ala Ala' Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys		
10		26	36
	Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val Cys His Ser		
		46	TGFA ⁵⁰ , PE ²⁵²
	Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu Leu Ala' Ala Met Ala Glu' Glu Gly		
15		263	273
	Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr		
		283	293
20	Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg		
		303	313
	Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg		
		323	333
25	Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro		
		343	353
	Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln		
30		363	373
	Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro		
		383	393
	Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn		
35		403	413
	Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly		
		423	433
40	Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Gln Arg Gln		
		443	453
	Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly		
45		463	473
	Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly		

50

55

TABLE 2 CONT'DTGF-alpha-PE₄₀ AMINO ACID SEQUENCE

5

483

493

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile

10

503

513

Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg

523

533

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His

15

543

553

Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Arg Leu Glu

563

573

20

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr

583

593

Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala

603

613

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Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys

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TABLE 3TGF-alpha-PE₄₀-αB AMINO ACID SEQUENCE

5	-4 -3 -2 -1' TGFa ¹	6	16
	Met Ala Ala Ala' Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys		
	26		36
10	Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val Cys His Ser		
	46	TGFa ⁵⁰ ,	'PE ²⁵²
	Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu Leu Ala'Met Ala Glu'Glu Gly Gly		
15	264		274
	Ser Leu Ala Ala Leu Thr Ala His Gln Ala Ala His Leu Pro Leu Glu Thr Leu Thr Arg		
	284		294
20	His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Ala Gly Tyr Pro Val Gln Arg Leu		
	304		314
	Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn		
	324		334
25	Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu		
	344		354
	Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly		
30	364		374
	Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val		
	384		394
	Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr		
35	404		414
	Pro Thr Glu Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr		
	424		434
40	Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr		
	444		454
	Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly		
	464		474
45	Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp		

50

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TABLE 3 CONT'DTGF- α PE₄₀ $\alpha\beta$ AMINO ACID SEQUENCE

5

484

494

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
504 514

10

Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
524 534

15

Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
544 554

20

Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Arg Leu Glu Thr
564 574

25

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
584 594

Pro Arg Asn Val Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
604 614

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TABLE 4TGF-alpha-PE₄₀ Ab AMINO ACID SEQUENCE

5	-4 -3 -2 -1' TGFA ¹	6	16
	Met Ala Ala Ala' Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys		
10	26		36
	Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val Cys His Ser		
	46	TGFA ⁵⁰ ,	PE ²⁵²
	Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu Leu Ala' Ala Met Ala Glu' Glu Gly		
15	263		273
	Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr		
	283		293
20	Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg		
	303		313
	Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg		
	323		333
25	Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro		
	343		353
	Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Glu Ser Glu Arg Phe Val Arg Gln		
30	363		373
	Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Thr Leu Thr Ala Pro		
	383		393
	Val Ala Ala Gly Glu Ala Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn		
35	403		413
	Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly		
	423		433
40	Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly		
	443		453
	Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly		
	463		473
45	Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly		

50

55

TABLE 4 CONT'DTGF-alpha-PE₄₀ Ab AMINO ACID SEQUENCE

5

483

493

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile
10 503 513

Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg
523 533

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His
15 543 553

Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Arg Leu Glu
563 573

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr
583 593

Asp Pro Arg Asn Val Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala
603 613

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys

30

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TABLE 5TGF-alpha-PE₄₀ ab AMINO ACID SEQUENCE

5	-4 -3 -2 -1' TGFa ¹	6	16
	Met Ala Ala Ala' Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys		
	26		36
10	Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val Cys His Ser		
	46	TGFa ⁵⁰ ,	' PE ²⁵²
	Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu Leu Ala'Met Ala Glu'Glu Gly Gly		
15	264		274
	Ser Leu Ala Ala Leu Thr Ala His Gln Ala Ala His Leu Pro Leu Glu Thr Leu Thr Arg		
	284		294
	His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Ala Gly Tyr Pro Val Gln Arg Leu		
20	304		314
	Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn		
	324		334
25	Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu		
	344		354
	Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly		
30	364		374
	Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Thr Leu Thr Ala Pro Val		
	384		394
	Ala Ala Gly Glu Ala Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr		
35	404		414
	Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr		
	424		434
40	Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr		
	444		454
	Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly		
	464		474
45	Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp		

50

55

TABLE 5 CONT'DTGF-alpha-PE₄₀ ab AMINO ACID SEQUENCE

5

484

494

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
504 514

10 Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
524 534

Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
554

15 Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Arg Leu Glu Thr
564 574

20 Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
584 594

Pro Arg Asn Val Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
604 614

25 Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys

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SEQUENCE LISTING

10

15 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGACCTCCT GGCTGCGCAT CTAGG

25

(2) INFORMATION FOR SEQ ID NO:2:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGGAGACGT TAACCCGTC

19

40

45

50

55

5

(2) INFORMATION FOR SEQ ID NO:3:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGACCTCCT GGCCATGGCC GAAGAGGGCG GCAGCCTGGC CGCGCTGACC GCGCACCAAGG	60
--	----

20 CTGCACACCT GCCGCTGGAG ACGTT	85
--	----

(2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AACCCGTCAT CGCCAGCCGC GCGGCTGGGA ACAACTGGAG CAGGCTGGCT ATCCGGTGCA	60
---	----

GCGGCTGGTC GCCCTCTACC TGGCGGCGCG GCTGTCTGG AACCAAGG	107
---	-----

35 (2) INFORMATION FOR SEQ ID NO:5:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGTGGTGA CCCTGAC	17
--------------------	----

50

55

5

(2) INFORMATION FOR SEQ ID NO:6:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGACCCCTGA CCGCGCCGGT CGCCGCCGCT GAAGCTGCAG GCC

43

20 (2) INFORMATION FOR SEQ ID NO:7:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30	ATGGCTGCAG CAGTGGTGTC CCATTTTAAT GACTGCCAG ATTCCCACAC TCAGTTCTGC	60
	TTCCCATGGAA CATGCAGGTT TTTGGTGCAG GAGGACAAGC CGGCATGTGT CTGCCATTCT	120
35	GGCTACGTTG GTGCGCCGCTG TGAGCATGCG GACCTCCTGG CTGCTATGGC CGAAGAGGGC	180
	GGCAGCCTGG CCGCGCTGAC CGCGCACCAAG GCTTGCCACC TGCCGCTGGA GACTTTAACCC	240
	CGTCATGCC AGCCGCGCGG CTGGGAACAA CTGGAGCAGT GCGGCTATCC GGTGCAGCGG	300
40	GCGTGGCCC TCTACCTGGC GGCGCGGCTG TCGTGGAACCC AGGTCGACCA GGTGATCCGC	360
	AACGCCCTGG CCAGCCCCGG CAGCGCCGGC GACCTGGCG AAGCGATCCG CGAGCAGCCG	420
	GAGCAGGCCG GTCTGGCCCT GACCCCTGGCC GCGGCCGAGA GCGAGCGCTT CGTCCGGCAG	480
45	GGCACCGGCA ACGACGAGGC CGGGCGGGCC AACGCCGACG TGGTGAGCCT GACCTGCCCG	540
	GTCGCCGCCG GTGAATGCGC GGGCCCGGCG GACAGCGCG ACGCCCTGCT GGAGCGCAAC	600
	TATCCCAC TG CGCGGAGTT CCTCGGGGAC GCGGGCGACG TCAGCTTCAG CACCCGGGC	660
	ACCGAGAACT GGACGGTGG A CGGGCTGCTC CAGGCGCAC ACCAACTGGG GGAGCGCGG	720
50	TATGTGTTCG TCGGCTACCA CGGCACCTTC CTCGAAGCGG CGCAAAGCAT CGTCTTCGGC	780
	GGGGTGCAGCG CGCGCAGCCA GGACCTCGAC GCGATCTGGC GCGGTTTCTA TATCGCCGGC	840

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	GATCCGGCGC TGGCCTACGG CTACGCCAG GACCAGGAAC CCGACGCACG CGGCCGGATC	900
10	CGCAACGGTG CCCTGCTGCG GGTCTATGTG CCGCGCTCGA GCCTGCCGGG CTTCTACCGC	960
	ACCAGCCTGA CCCTGGCCGC GCCGGAGGCG GCGGGCGAGG TCGAACGGCT GATCGGCCAT	1020
	CCGCTGCCGC TCGCCTCGGA CGCCATCACCC GCCCCCGAGG AGGAAGGCGG GCGCCTGGAG	1080
15	ACCATTCTCG GCTGGCCGCT GGCCGAGCGC ACCGTGGTGA TTCCCTCGGC GATCCCCACC	1140
	GACCCGCGCA ACACCGCCGG CGACCTCGAC CCGTCCAGCA TCCCCCACAA GGAACAGGCG	1200
	ATCAGCGCCC TGCCGGACTA CGCCAGCCAG CCCGGCAAAC CGCCGCGCGA GGACCTGAAG	1260
	TAA	1263

20 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30	Met Ala Ala Ala Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His	1	5	10	15
	Thr Gln Phe Cys Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp	20	25	30	
35	Lys Pro Ala Cys Val Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu	35	40	45	
	His Ala Asp Leu Leu Ala Ala Met Ala Glu Glu Gly Ser Leu Ala	50	55	60	
40	Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr	65	70	75	80
	Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr	85	90	95	
45	Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp	100	105	110	
	Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser	115	120	125	
50	Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg	130	135	140	

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(2) INFORMATION FOR SEQ ID NO:9:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 419 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	Met Ala Ala Ala Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His				
1	5	10	15		
20	Thr Gln Phe Cys Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp	20	25	30	
	Lys Pro Ala Cys Val Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu	35	40	45	
25	His Ala Asp Leu Leu Ala Met Ala Glu Glu Gly Ser Leu Ala Ala	50	55	60	
	Leu Thr Ala His Gln Ala Ala His Leu Pro Leu Glu Thr Leu Thr Arg	65	70	75	80
30	His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Ala Gly Tyr Pro	85	90	95	
	Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn	100	105	110	
35	Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly	115	120	125	
	Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu	130	135	140	
40	Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly	145	150	155	160
	Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu	165	170	175	
45	Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly	180	185	190	
	Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Glu Ala Glu Phe Leu Gly	195	200	205	
50	Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr	210	215	220	
	Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr	225	230	235	240

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Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile
 245 250 255
 Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp
 260 265 270
 Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala
 275 280 285
 Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu
 290 295 300
 Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
 305 310 315 320
 Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu
 325 330 335
 Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu
 340 345 350
 Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu
 355 360 365
 Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val
 370 375 380
 Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
 385 390 395 400
 Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu
 405 410 415
 Asp Leu Lys

(2) INFORMATION FOR SEO ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

iii) MOLECULE TYPE: protein

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5 Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile
 245 250 255
 10 Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp
 260 265 270
 15 Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala
 275 280 285
 20 Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu
 290 295 300
 25 Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
 305 310 315 320
 30 Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu
 325 330 335
 35 Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu
 340 345 350
 40 Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu
 355 360 365
 45 Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val
 370 375 380
 50 Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
 385 390 395 400
 55 Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu
 405 410 415
 60 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5 Met Ala Ala Ala Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His
 1 5 10 15
 Thr Gln Phe Cys Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp
 10 20 25 30
 Lys Pro Ala Cys Val Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu
 15 35 40 45
 His Ala Asp Leu Leu Ala Ala Met Ala Glu Glu Gly Ser Leu Ala
 20 50 55 60
 Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
 25 65 70 75 80
 Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
 30 85 90 95
 Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
 35 100 105 110
 Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser
 40 115 120 125
 Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg
 45 130 135 140
 Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln
 50 145 150 155 160
 Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Thr
 55 165 170 175
 Leu Thr Ala Pro Val Ala Ala Gly Glu Ala Ala Gly Pro Ala Asp Ser
 60 180 185 190
 Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
 65 195 200 205
 Gly Asp Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
 70 210 215 220
 Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly
 75 225 230 235 240
 Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
 80 245 250 255
 Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
 85 260 265 270
 Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
 90 275 280 285
 Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala
 95 290 295 300

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Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg
 305 310 315 320
 Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
 10 325 330 335
 Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
 340 345 350
 Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
 15 355 360 365
 Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
 370 375 380
 Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala
 20 385 390 395 400
 Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg
 405 410 415
 Glu Asp Leu Lys
 25 420

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 419 amino acids
 30 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ala Ala Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His
 1 5 10 15

40 Thr Gln Phe Cys Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp
 20 25 30

Lys Pro Ala Cys Val Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu
 35 40 45

45 His Ala Asp Leu Leu Ala Met Ala Glu Glu Gly Gly Ser Leu Ala Ala
 50 55 60

Leu Thr Ala His Gln Ala Ala His Leu Pro Leu Glu Thr Leu Thr Arg
 65 70 75 80

50 His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Ala Gly Tyr Pro
 85 90 95

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Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn
 100 105 110
 Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly
 115 120 125
 Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu
 130 135 140
 Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly
 145 150 155 160
 Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val Thr Leu
 165 170 175
 Thr Ala Pro Val Ala Ala Gly Glu Ala Ala Gly Pro Ala Asp Ser Gly
 180 185 190
 Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly
 195 200 205
 Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr
 210 215 220
 Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr
 225 230 235 240
 Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile
 245 250 255
 Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp
 260 265 270
 Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala
 275 280 285
 Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu
 290 295 300
 Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
 305 310 315 320
 Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu
 325 330 335
 Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu
 340 345 350
 Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu
 355 360 365
 Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val
 370 375 380
 Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
 385 390 395 400

Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu
405 410 415

5 Asp Leu Lys

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Claims

1. The use, for the manufacture of a medicament for treating bladder cancer cells, of a hybrid protein comprising a cell targeting agent selected from a member of the EGF family of peptide hormones that bind to the EGF receptor on bladder tumor cells, and a cell toxin selected from a member of the ADP-ribosylating class of mammalian cell poisons, the amount of hybrid protein being effective to kill bladder cancer cells.
2. The use according to Claim 1 wherein the cell targeting agent is EGF or TGF-alpha, and the cell toxin is PE₄₀ AB, PE₄₀ Ab, PE₄₀ aB, PE₄₀ ab, diphtheria toxin or ricin toxin.
3. The use according to Claim 1 wherein the hybrid protein is in the form of a solution or suspension in a physiologically acceptable liquid.
4. The use according to Claim 3 wherein the liquid is sterile water, water for injection, saline or buffered saline optionally containing a carrier protein.
5. The use according to Claim 4 wherein the liquid is phosphate buffered saline optionally containing human serum albumin.
6. The use according to Claim 3 wherein the physiologically acceptable liquid contains from about 0.1 mg to about 10 mg of the hybrid protein per 60 ml.
7. The use according to Claim 3 wherein the physiologically acceptable liquid contains from about 0.5 mg to about 5 mg of the hybrid protein per 60 ml.
8. The use according to Claim 3 wherein the physiologically acceptable liquid contains from about 2 mg to about 4 mg of the hybrid protein per 60 ml.
9. The use according to Claim 3 wherein the contacting is continued for a period of from about 30 minutes to about 4 hours.
10. The use according to Claim 4 wherein the phosphate buffered saline contains from about 0.1 mg to about 10 mg of hybrid protein per 60 ml.
11. The use according to Claim 4 wherein the phosphate buffered saline contains from about 0.5 mg to about 5 mg of the hybrid protein per 60 ml
12. The use according to Claim 4 wherein the phosphate buffered saline contains from about 2 mg to about 4 mg of the hybrid protein per 60 ml.
13. The use according to Claim 3 wherein the medicament is adapted for contacting bladder cancer cells at ambient temperature.
14. A composition comprising a physiologically acceptable liquid containing a concentration of hybrid protein TGF-alpha - PE₄₀ aB, TGF-alpha - PE₄₀ Ab or TGF-alpha - PE₄₀ ab that is effective to kill bladder cancer cells.

15. A composition according to Claim 14 that contains from about 0.1 mg to about 10 mg of the hybrid protein per 60 ml.
- 5 16. A composition according to Claim 14 that contains from about 0.5 mg to about 5 mg of the hybrid protein per 60 ml.
17. A composition according to Claim 14 that contains from about 2 mg to about 4 mg of the hybrid protein per 60 ml.
- 10 18. A composition according to Claim 14 wherein the liquid is phosphate buffered saline optionally containing a carrier protein.
19. A composition according to Claim 18 wherein the optional carrier protein is human serum albumin.
- 15 20. Hybrid proteins TGF-alpha - PE₄₀ aB, TGF-alpha - PE₄₀ Ab or TGF-alpha - PE₄₀ ab of enhanced potency prepared by a process comprising precipitating with sulfate one of the foregoing hybrid proteins that has been expressed in a transformed cell, and purifying the hybrid protein by affinity chromatography using a metal-chelating column, and not subjecting the hybrid protein to treatment with urea.
- 20 21. A hybrid protein according to Claim 20 wherein the precipitating sulfate is (NH₄)₂SO₄.

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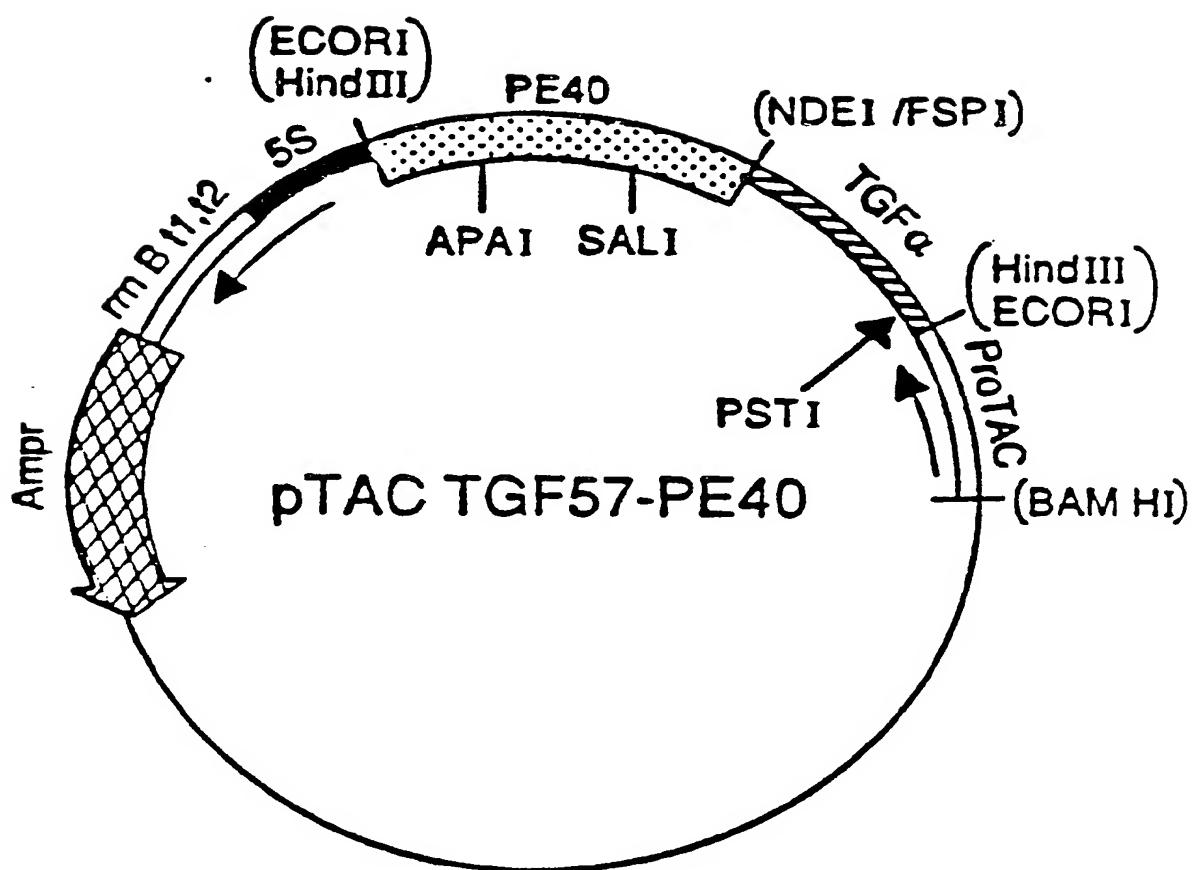
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FIGURE 1





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(54) Method of treating bladder cancer cells.

(57) We have modified PE₄₀ toxin by removing at least two of its four cysteine amino acid residues and have formed hybrid molecules containing modified PE₄₀ linked to TGF-alpha and have found that these hybrid molecules have utility in killing bladder cancer cells.

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